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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 05:34:19 ; Search time 9440 Seconds
(without alignments)
11588.752 Million cell updates/sec

Title: US-09-989-734-A-351
Perfect score: 2524
Sequence: 1 cgccaagcatgcagtaaagg.....ataaagcctttgcaagataa 2524

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

AX697283

LOCUS AX697283 2524 bp DNA linear PAT 02-APR-2003

DEFINITION Sequence 351 from Patent WO0078961.

ACCESSION AX697283

VERSION AX697283.1 GI:29498434

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0078961-A 351 28-DEC-2000;
Genentech Inc. (US)

FEATURES Location/Qualifiers

source 1. .2524
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	361	TACCCCTGGGCTATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGACCCCAAC	420
Db	361	 TACCCCTGGGCTATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGACCCCAAC	420
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Qy	481	CACCCCAACTCAGACTCCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGCACCT	540
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RESULT 2

AY358534

LOCUS AY358534 2524 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA76396 ESRM828 (UNQ828) mRNA, complete cds.

ACCESSION AY358534

VERSION AY358534.1 GI:37182190

KEYWORDS FLI_CDNA.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2524)
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
 Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
 PUBMED 12975309

REFERENCE 2 (bases 1 to 2524)
 AUTHORS Clark,H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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ORIGIN

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Db	1381	CTCCTGGCTCCTGCCCCCTTGACACACCACCGGAACACTCCCCAGCCCCACGGGCAATCCT	1440
QY	1441	ATCTGCTCGCCCTCCTGCAGGTGGGGGCCTCACATATCTGTGACTTCGGGTCCCTGTCCC	1500
Db	1441	ATCTGCTCGCCCTCCTGCAGGTGGGGGCCTCACATATCTGTGACTTCGGGTCCCTGTCCC	1500
QY	1501	CACCCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCACAGGCCATTTG	1560
Db	1501	CACCCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCACAGGCCATTTG	1560
QY	1561	CACACGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGTGACTCTCATGTTCT	1620
Db	1561	CACACGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGTGACTCTCATGTTCT	1620
QY	1621	CTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAGTGGTCA	1680
Db	1621	CTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAGTGGTCA	1680
QY	1681	GCGTTTCCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGGTGTG	1740
Db	1681	GCGTTTCCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGGTGTG	1740
QY	1741	CGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCCGAGCCCCCTGCGT	1800
Db	1741	CGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCCGAGCCCCCTGCGT	1800

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 11:46:45 ; Search time 108 Seconds
(without alignments)
6361.382 Million cell updates/sec

Title: US-09-989-734-356
Perfect score: 1238
Sequence: 1 gcgacgggcaggacgccccg.....caaaaaaaaaaaaaaaaaaaaaa 1238

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	71.4	5.8	82	4	US-09-833-381-83	Sequence 83, Appl		
2	68	5.5	5102	1	US-08-494-168-1	Sequence 1, Appli		
3	66.8	5.4	579	4	US-09-404-879A-273	Sequence 273, App		
4	66.8	5.4	579	4	US-09-338-933-273	Sequence 273, App		
5	66.8	5.4	579	4	US-09-215-681-273	Sequence 273, App		
6	66.8	5.4	579	4	US-09-216-003A-273	Sequence 273, App		
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c 9	65.6	5.3	330	4	US-09-404-879A-274	Sequence 274, App		
c 10	65.6	5.3	330	4	US-09-338-933-274	Sequence 274, App		
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	13	64.6	5.2	3120	4	US-09-169-768-29	Sequence 29, Appl
	14	63.8	5.2	444	4	US-09-397-787-161	Sequence 161, App
	15	63.6	5.1	1839	1	US-08-383-744-1	Sequence 1, Appli
	16	63.6	5.1	1839	2	US-08-999-336-1	Sequence 1, Appli
	17	63.6	5.1	1839	5	PCT-US96-01427-1	Sequence 1, Appli
c	18	63.6	5.1	7218	1	US-08-232-463-14	Sequence 14, Appl
	19	63	5.1	801	4	US-09-404-879A-216	Sequence 216, App
	20	63	5.1	801	4	US-09-338-933-216	Sequence 216, App
	21	63	5.1	801	4	US-09-215-681-216	Sequence 216, App
	22	63	5.1	801	4	US-09-216-003A-216	Sequence 216, App
	23	62.6	5.1	855	4	US-09-552-204A-10	Sequence 10, Appl
	24	62.6	5.1	1341	2	US-08-945-848-7	Sequence 7, Appli
	25	62.6	5.1	2363	2	US-08-945-848-6	Sequence 6, Appli
	26	62	5.0	3170	4	US-09-169-768-1	Sequence 1, Appli
	27	61.4	5.0	3171	4	US-09-169-768-15	Sequence 15, Appl
	28	61.4	5.0	3181	1	US-08-655-086-1	Sequence 1, Appli
	29	61.4	5.0	3349	4	US-09-169-768-13	Sequence 13, Appl
	30	61.4	5.0	3541	4	US-09-169-768-9	Sequence 9, Appli
	31	61.4	5.0	4409	4	US-09-331-347C-22	Sequence 22, Appl
	32	61.2	4.9	369	4	US-09-535-521-24	Sequence 24, Appl
c	33	61.2	4.9	369	4	US-09-535-521-26	Sequence 26, Appl
	34	61.2	4.9	384	4	US-09-535-521-7	Sequence 7, Appli
c	35	61.2	4.9	384	4	US-09-535-521-9	Sequence 9, Appli
	36	61.2	4.9	417	4	US-09-535-521-10	Sequence 10, Appl
c	37	61.2	4.9	417	4	US-09-535-521-12	Sequence 12, Appl
	38	61.2	4.9	423	4	US-09-535-521-13	Sequence 13, Appl
c	39	61.2	4.9	423	4	US-09-535-521-15	Sequence 15, Appl
	40	61.2	4.9	561	4	US-09-535-521-16	Sequence 16, Appl
c	41	61.2	4.9	561	4	US-09-535-521-18	Sequence 18, Appl
	42	61.2	4.9	624	4	US-09-535-521-19	Sequence 19, Appl
c	43	61.2	4.9	624	4	US-09-535-521-21	Sequence 21, Appl
	44	61.2	4.9	876	4	US-09-535-521-4	Sequence 4, Appli
c	45	61.2	4.9	876	4	US-09-535-521-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-833-381-83

; Sequence 83, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 83

; LENGTH: 82

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 5.8%; Score 71.4; DB 4; Length 82;
Best Local Similarity 92.6%; Pred. No. 4.6e-09;
Matches 75; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 801 GGTGGCCTCGGGCGGCTGGAA 821
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 Db 61 GGTGGCCTCGGGAAAATGGAA 81

US-08-494-168-1

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; Sequence 1, Application US/08494168
; Patent No. 5731192
; GENERAL INFORMATION:
;   APPLICANT:  Reeder, Stephen T.
;   APPLICANT:  Zhou, Jing
;   TITLE OF INVENTION:  Collagen COL4A6: Gene, Protein and Method
;   TITLE OF INVENTION:  of Detecting Collagen Deficiency
;   NUMBER OF SEQUENCES:  10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Foley & Lardner
;     STREET:    3000 K Street, N.W., Suite 500
;     CITY:      Washington, D.C.
;     COUNTRY:   USA
;     ZIP:       20007-5109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/494,168
;     FILING DATE:
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/112,465
;     FILING DATE:  27-AUG-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  SAXE, Bernhard D.
;     REGISTRATION NUMBER:  28,665
;     REFERENCE/DOCKET NUMBER:  40397/104/BABR
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (202)672-5300
;     TELEFAX:   (202)672-5399
;     TELEX:     904136
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5102 base pairs
;       TYPE:    nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(2..82, 86..97, 101..4399, 4403..4420, 4424
; LOCATION: ..4465, 4469..4876, 4880..5101)
US-08-494-168-1

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Best Local Similarity 56.8%; Pred. No. 1.9e-07;
Matches 125; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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Qy      185 CTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGACGGCCTGGAA 244
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Db      2913 CTGGACGCGCTGGTACTCCTGGTGAAGGGAGACAGAGGCAATCCGGGGCCAGTCGGAA 2972

Qy      245 GAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGG 304
          | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2973 TACCTAGTCCAAGACGTCCAATGTCAAACCTTTGGCTCAAAGGAGACAAAGGCTCTCAAG 3032

Qy      305 GTCGTCATGGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACA 364
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Db      3033 GCTCAGCCGGATCCAATGGATTTCTGGGCCAAGAGGTGACAAAGGAGAGGCTGGTCGAC 3092

Qy      365 TAGGACCCCCTGGTCTTAATGGAGAACCAGGCCTCCCATG 404
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Db      3093 CTGGACCACCAGGCCTACCTGGAGCTCCTGGCCTCCAGG 3132

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RESULT 3

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US-09-404-879A-273
; Sequence 273, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 273
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(579)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-273

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Query Match          5.4%; Score 66.8; DB 4; Length 579;
Best Local Similarity 52.0%; Pred. No. 1.5e-07;
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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Qy      117 GTCAGTCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGAT 176

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Db      7  GTCGCGGCCGAGGTCTGGCCCTCCTGGCAAGGCTGGTGAAGATGGTCACCCCTGGAAAACC 66

Qy      177 CCTCGTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACG 236
      | |||| | ||| | || | ||| | |||| | || | ||| |||
Db      67  CGGACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCCTGGAAC 126

Qy      237 GCCTGGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGG 296
      ||||| | ||| || || | ||| ||| || | ||| ||| ||
Db      127 TCCTGGACTTCCTGGCTTCAAAGGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGG 186

Qy      297 CAGTGTGGGTGCTCATGGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTC 356
      ||| || ||| | ||| ||| | |||| | ||| ||| ||
Db      187 ACAGCCCGGTGCTCCTGGTGTGAAGGTGAACCTGGNGCCCTGGTGAAAATGGAAGTCC 246

Qy      357 CGGTGACATAGGACCCCTGGTCCTAATGGAGAACCAGGCC 397
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RESULT 4

US-09-338-933-273

; Sequence 273, Application US/09338933

; Patent No. 6488931

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer Lynn

; APPLICANT: King, Gordon E.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF

; TITLE OF INVENTION: OVARIAN CANCER

; FILE REFERENCE: 210121.462C1

; CURRENT APPLICATION NUMBER: US/09/338,933

; CURRENT FILING DATE: 1999-06-23

; NUMBER OF SEQ ID NOS: 312

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 273

; LENGTH: 579

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(579)

; OTHER INFORMATION: n = A,T,C or G

US-09-338-933-273

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Best Local Similarity 52.0%; Pred. No. 1.5e-07;

Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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Qy      177 CCTCGTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACG 236
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Qy      237 GCCTGGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGG 296

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 11:45:05 ; Search time 5092 Seconds
(without alignments)
10537.839 Million cell updates/sec

Title: US-09-989-734-356
Perfect score: 1238
Sequence: 1 gcgacgggcaggacgccccg.....caaaaaaaaaaaaaaaaaaaaaa 1238

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Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%
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 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	1238	100.0	1238	6	AX491060	AX491060 Sequence
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6	1226.8	99.1	1248	9	BC000078	BC000078 Homo sapi
7	1142.6	92.3	1417	9	BC009951	BC009951 Homo sapi
8	1132	91.4	1341	6	BD103302	BD103302 Novel col
9	978	79.0	1269	6	BD103330	BD103330 Novel col
10	978	79.0	1269	6	BD103331	BD103331 Novel col
11	950.6	76.8	1139	6	BD103303	BD103303 Novel col
12	877	70.8	1067	6	BD103305	BD103305 Novel col
13	834	67.4	1197	6	BD103329	BD103329 Novel col
14	832.2	67.2	1067	6	BD103306	BD103306 Novel col
15	813	65.7	813	6	BD103332	BD103332 Novel col
16	805.6	65.1	995	6	BD103304	BD103304 Novel col
17	733.4	59.2	139357	9	AC010907	AC010907 Homo sapi
18	686.6	55.5	735	6	BD103333	BD103333 Novel col
19	675.4	54.6	1522	6	BD103307	BD103307 Novel col
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25	545.2	44.0	669	6	BD103339	BD103339 Novel col
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31	322.2	26.0	246539	2	AC125638	AC125638 Rattus no
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	37	226.4	18.3	212049	5	BX005484	BX005484 Zebrafish
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	43	154.8	12.5	166900	2	AC115924	AC115924 Mus muscu
	44	154.8	12.5	222510	2	AC123656	AC123656 Mus muscu
	45	154.8	12.5	345420	2	AC131337	AC131337 Mus muscu

ALIGNMENTS

RESULT 1

AR252616

LOCUS	AR252616	1238 bp	DNA	linear	PAT 20-DEC-2002
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DEFINITION Sequence 356 from patent US 6478825.

ACCESSION AR252616

VERSION AR252616.1 GI:27300524

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1238)

AUTHORS Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.

TITLE Implant, method of making same and use of the implant for the
 treatment of bone defects

JOURNAL Patent: US 6478825-A 356 12-NOV-2002:

FEATURES	Location/Qualifiers
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source      1.  .1238
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/organism="unknown"
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/mol type="genomic DNA"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4e-210;

Matches 1238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCCTGCCTGCG 60

Qy 61 CTCAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA 120

Db 61 CTCAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA 120

Qy 121 CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC 180

Db 121 CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC 180

Qy 181 GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGACGGCCT 240

Db 181 GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCT 240

Qy		241 GGAAGAGTCGGCCCCACGCGGAGAAAAAGGAGACATGGGGGACAAAGGCAGAAAAGGCAGT	300
Db		241 GGAAGAGTCGGCCCCACGCGGAGAAAAAGGAGACATGGGGGACAAAGGCAGAAAAGGCAGT	300
Qy		301 GTGGGTCTGTCATGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Db		301 GTGGGTCTGTCATGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Qy		361 GACATAGGACCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGACGCCAGCTG	420
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Qy		421 CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Db		421 CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Qy		481 ATCAAGAATGCTGTCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Db		481 ATCAAGAATGCTGTCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Qy		541 GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCTTCCAGGGCCGCGGGGGCACGCTGAGC	600
Db		541 GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCTTCCAGGGCCGCGGGGGCACGCTGAGC	600
Qy		601 ATGCCCAAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Db		601 ATGCCCAAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Qy		661 GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Db		661 GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Qy		721 CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Db		721 CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Qy		781 GAGGAGGACTGCGTGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Db		781 GAGGAGGACTGCGTGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Qy		841 ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Db		841 ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Qy		901 CCATTGGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC	960
Db		901 CCATTGGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC	960
Qy		961 CAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT	1020
Db		961 CAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT	1020
Qy		1021 AAAC TGAGAAAATGGCCTATGCTTAAGAGGAAAATGAAAGTGTTCTGGGGTGCTGTCTC	1080
Db		1021 AAAC TGAGAAAATGGCCTATGCTTAAGAGGAAAATGAAAGTGTTCTGGGGTGCTGTCTC	1080

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Qy      1081 TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140
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Db      1081 TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140

Qy      1141 CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATAACAATAAAATCTTTAAG 1200
          |||
Db      1141 CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATAACAATAAAATCTTTAAG 1200

Qy      1201 TAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA 1238
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Db      1201 TAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA 1238

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RESULT 2

AX403469

LOCUS AX403469 1238 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 356 from Patent WO0073454.

ACCESSION AX403469

VERSION AX403469.1 GI:21436970

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0073454-A 356 07-DEC-2000;
Genentech Inc. (US)

FEATURES

source

Location/Qualifiers

1. .1238

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1238; DB 6; Length 1238;

Best Local Similarity 100.0%; Pred. No. 1.4e-210;

Matches 1238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCGACGGGCAGGACGCCCCGTTTCGCTAGCGCGTCTCAGGAGTTGGTGTCTGCCTGCG 60
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Db      1 GCGACGGGCAGGACGCCCCGTTTCGCTAGCGCGTCTCAGGAGTTGGTGTCTGCCTGCG 60

Qy      61 CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA 120
          |||
Db      61 CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA 120

Qy      121 CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC 180
          |||
Db      121 CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC 180

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Qy	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCT	240
Db	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCT	240
Qy	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Db	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Qy	301	GTGGGTCGTCATGGA AAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Db	301	GTGGGTCGTCATGGA AAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Qy	361	GACATAGGACCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Db	361	GACATAGGACCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Qy	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Db	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Qy	481	ATCAAGAATGCTGTGCGCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Db	481	ATCAAGAATGCTGTGCGCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Qy	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Db	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Qy	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Db	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Qy	661	GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Db	661	GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Qy	721	CACTCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Db	721	CACTCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Qy	781	GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Db	781	GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Qy	841	ACCATGTACTTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Db	841	ACCATGTACTTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Qy	901	CCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC	960
Db	901	CCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC	960
Qy	961	CAGCCAGGGAGCTGTCCCTCTGTGAAGGTTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT	1020
Db	961	CAGCCAGGGAGCTGTCCCTCTGTGAAGGTTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT	1020
Qy	1021	AAACTGAGAAAATGGCCTATGCTTAAGAGGAAAAATGAAAGTGTTCTGGGGTGCTGTCTC	1080

Qy	61	CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA	120
Db	61	CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA	120
Qy	121	CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC	180
Db	121	CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC	180
Qy	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCT	240
Db	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCT	240
Qy	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Db	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Qy	301	GTGGGTCGTTCATGGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Db	301	GTGGGTCGTTCATGGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Qy	361	GACATAGGACCCCTGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Db	361	GACATAGGACCCCTGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Qy	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Db	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Qy	481	ATCAAGAATGCTGTGCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Db	481	ATCAAGAATGCTGTGCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Qy	541	GAGGAGAAGCGCTACGCGGACGCCAGCTGTCTCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Db	541	GAGGAGAAGCGCTACGCGGACGCCAGCTGTCTCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Qy	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Db	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Qy	661	GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Db	661	GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Qy	721	CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Db	721	CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Qy	781	GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Db	781	GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Qy	841	ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Db	841	ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
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Db      961 CAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT 1020
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Db      1021 AAAC TGAGAAAATGGCCTATGCTTAAGAGGAAAATGAAAGTGTTCCTGGGGTGCTGTCTC 1080
Qy      1081 TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140
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Db      1081 TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140
Qy      1141 CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATAACAATAAAATCTTTAAG 1200
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Db      1141 CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATAACAATAAAATCTTTAAG 1200
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RESULT 4

AX491060

LOCUS AX491060 1238 bp DNA linear PAT 16-AUG-2002

DEFINITION Sequence 167 from Patent WO0200690.

ACCESSION AX491060

VERSION AX491060.1 GI:22323867

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 167 03-JAN-2002;
Genentech, Inc. (US)

FEATURES

Location/Qualifiers

source

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/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 1238; DB 6; Length 1238;
Best Local Similarity 100.0%; Pred. No. 1.4e-210;
Matches 1238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	CTCAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA	120
Qy	121	CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC	180
Db	121	CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC	180
Qy	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGACGGCCT	240
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Qy	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Db	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
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Db	301	GTGGGTCGTCATGGA AAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Qy	361	GACATAGGACCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Db	361	GACATAGGACCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
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Db	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
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Qy	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Db	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
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Db	661	GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Qy	721	CACTCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
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